

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 7,250,165 B2
APPLICATION NO. : 09/920137
DATED : July 31, 2007
INVENTOR(S) : Heavner et al.

Page 1 of 27

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column 73

Line 21, delete the entire sequence listing through column 84, line 19, and insert

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SEQUENCE LISTING

<210> 1

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> Heavy Chain complementarity determinng region 1 (CDR1).

<400> 1

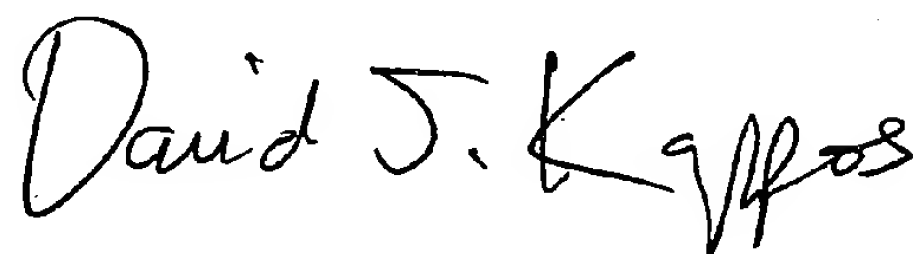
Ser Tyr Ala Met His

1

5

Signed and Sealed this

Tenth Day of August, 2010



David J. Kappos
Director of the United States Patent and Trademark Office

<210> 2

<211> 17

<212> PRT

<213> Homo sapiens

<220>

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<222> (1) .. (17)

<223> Heavy Chain complementarity determinng region 2 (CDR2).

<220>

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<222> (1) .. (1)

<223> Xaa at position 1 is selected from Ile, Phe or Val.

<220>

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<222> (2) .. (2)

<223> Xaa at position 2 is selected from Ile or Met.

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa at position 3 is selected from Ser or Leu.

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa at position 4 is selected from Tyr or Phe.

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa at position 10 is selected from Lys or Tyr.

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> Xaa at position 11 is selected from Ser or Tyr.

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Xaa at position 17 is selected from Asp or Gly.

<400> 2

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Asp | Gly | Ser | Asn | Lys | Xaa | Xaa | Ala | Asp | Ser | Val | Lys | Xaa |
| 1 | | | | | 5 | | | | | 10 | | | | | 15 | |

<210> 3

<211> 17

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(17)

<223> Heavy Chain complementarity determinng region 3 (CDR3).

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<222> (4) .. (4)
<223> Xaa at position 4 is selected from Ile or Val.

<220>
<221> MISC_FEATURE
<222> (5) .. (5)
<223> Xaa at position 5 is selected from Ser, Ala or Gly.

<220>
<221> MISC_FEATURE
<222> (9) .. (9)
<223> Xaa at position 9 is selected from Asn or Tyr.

<400> 3

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Gly | Xaa | Xaa | Ala | Gly | Gly | Xaa | Tyr | Tyr | Tyr | Tyr | Gly | Met | Asp | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |

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<211> 11

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 $\langle 220 \rangle$

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 $\langle 222 \rangle \quad (1) \dots (11)$

<223> Light Chain complementarity determininng region 1 (CDR1).

<220>

<221> MISC_FEATURE

<222> (7) . . (7)

<223> Xaa at position 7 is selected from Ser or Tyr.

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Arg Ala Ser Gln Ser Val Xaa Ser Tyr Leu Ala

1

5

10

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<223> Light Chain complementarity determinng region 2 (CDR2).

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1 5

<210> 6

 $\langle 211 \rangle$ 10

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<222> (1) . . (10)

<223> Light Chain complementarity determinng region 3 (CDR3).

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1 5 10

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<400> 7

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Val
 35 40 45

Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 8

<211> 108

<212> PRT

<213> Homo sapiens

<400> 8

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 9
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<220>
<221> MISC_FEATURE
<222> (1)..(157)
<223> human TNF alpha monomer sequence

<400> 9

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Ser | Ser | Ser | Arg | Thr | Pro | Ser | Asp | Lys | Pro | Val | Ala | His | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| | | | | | | | | | | | | | | | |
| Val | Ala | Asn | Pro | Gln | Ala | Glu | Gly | Gln | Leu | Gln | Trp | Leu | Asn | Arg | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| | | | | | | | | | | | | | | | |
| Ala | Asn | Ala | Leu | Leu | Ala | Asn | Gly | Val | Glu | Leu | Arg | Asp | Asn | Gln | Leu |
| | | | 35 | | | | 40 | | | | | 45 | | | |

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
85 90 95

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
100 105 110

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
115 120 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

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<211> 18

<212> DNA

<213> Homo sapiens

<400> 10

ttggtccagt cggactgg 18

<210> 11

<211> 18

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<400> 11

cacctgcact cggtgctt 18

<210> 12
<211> 30
<212> DNA
<213> Homo sapiens

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cactgttttg agtgtgtacg ggcttaagtt 30

<210> 13
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<213> Homo sapiens

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gccgcacgtg tggaaggg 18

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<213> Homo sapiens

<400> 14

agtcaaggtc ggactggctt aagtt

25

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<212> DNA

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<400> 15

gttggtccct ctcacaatct tcgaattt

28

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<212> DNA
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<400> 17

Met Asp Trp Thr Trp Ser Ile
1 5

<210> 18
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<400> 18

tttcgtacgc caccatggac tggacctgga gcatc 35

<210> 19
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<212> DNA
<213> Homo sapiens

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tttcgtacgc caccatgggg ttggggctga gctg 34

<210> 20
<211> 35
<212> DNA
<213> Homo sapiens

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tttcgtacgc caccatggag ttggtgga gcatg 35

<210> 21
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<400> 21

tttcgtacgc caccatgaaa cacctgtggt tcttc 35

<210> 22
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<400> 22

tttcgtacgc caccatgggg tcaaccgcca tcttc 35

<210> 23
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<212> PRT
<213> Homo sapiens

<400> 23

Thr Val Thr Val Ser Ser
1 5

<210> 24
<211> 36
<212> DNA
<213> Homo sapiens

<400> 24

gtgccagtgg cagaggagtc cattcaagct taagtt 36

<210> 25
<211> 5
<212> PRT
<213> Homo sapiens

<400> 25

Met Asp Met Arg Val
1 5

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<212> DNA
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<400> 26

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<210> 27
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<212> DNA
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<400> 27

tttgtcgaca ccatggaagc cccagctc 28

<210> 28

<211> 6

<212> PRT

<213> Homo sapiens

<400> 28

Thr Lys Val Asp Ile Lys

1 5

<210> 29

<211> 41

<212> DNA

<213> Homo sapiens

<400> 29

ctggtttcac ctatagtttg cattcagaat tcggcgccctt t

41

<210> 32

<211> 19

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<221> MISC_FEATURE

<222> (1) . . (19)

<223> Signal sequence for heavy chain variable region sequences as presented in original Figure 4

<400> 32

Met Gly Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly

1 5 10 15

Val Gln Cys

<210> 33

<211> 20

<212> PRT

<213> Homo sapiens

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<222> (1)..(20)

<223> Signal sequence for light chain variable region sequences as presented in original Figure 5

<400> 33

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro

1

5

10

15

Asp Thr Thr Gly

20

<210> 34

<211> 428

<212> DNA

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<222> (1)..(421)

<223> heavy chain variable region DNA sequences as presented in original Figure 2A-2B

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tgtgcagcct ctggttcacc ttcagtagct atgctatgca ctgggtccgc caggctccgg 180
caaggggctg gagtgggtgg cagttatatc atatgatgga aaataaatac tacgcagact 240
ccgtgaaggg ccgattcacc atctagagac aattccaaga acacgctgta tctgcaaata 300
aacagccaga gctgaggaca cggctgtgta ttactgtgcg agagatcgag gtatatcagc 360
aggtggaata ctactactac tacggtatgg acgtctgggg gcaagggacc acggtcaccg 420
tctcctca                                         428
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<210> 35

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(387)

<223> light chain variable region DNA sequences as presented in original Figure 3

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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca gagtgtttag agctacttag cctggtacca acagaaacct 180
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 240
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 300
gaagattttg cagtttatta ctgtcagcag cgtagcaact ggctccatt cactttcggc 360
cctgggacca aagtggatat caaacgt                                     387
```

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